

**AMENDMENTS TO THE CLAIMS**

1. (Cancelled)
2. (Currently amended) The A method of claim 3 identifying candidate genes involved in systemic lupus erythematosus (SLE), comprising identifying a region of the genome adjacent to an SLE-associated marker, and selecting any gene in the region having a distance between the first nucleotide of the gene and the first nucleotide of an L1 element of less than about 200,000 base pairs as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least about 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
3. (Currently amended) A method of identifying candidate genes involved in ~~systemic lupus erythematosus ( SLE )~~, comprising identifying a region of the genome adjacent to ~~a disease~~ an SLE-associated marker, and selecting any gene in the region containing an L1 element in an intronic region or in a 5' or 3' regulatory region as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
- 4-18. (Cancelled)
19. (Currently amended) The method of claim 2 3, comprising selecting any gene containing an L1 element in an intronic region as a candidate gene involved in SLE.
20. (Currently amended) The method of claim 2 3, comprising selecting any gene containing an L1 element in a 5' regulatory region as a candidate gene involved in SLE.

21. (Currently amended) The method of claim 2 ~~3~~, comprising selecting any gene containing an L1 element in a 3' regulatory region as a candidate gene involved in SLE.
22. (Previously added) The method of claim 2, wherein the L1 element has at least about 98% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
23. (Previously added) The method of claim 2, wherein the L1 element has at least about 99% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
24. (Canceled) ~~The method of claim 2, wherein the distance between the first nucleotide of the L1 element and the first nucleotide of the gene is less than about 200,000 base pairs.~~
25. (Previously added) The method of claim 2, wherein the distance between the first nucleotide of the L1 element and the first nucleotide of the gene is less than about 100,000 base pairs.
26. (New) The method of claim 2, wherein the L1 element comprises residues 1-884 of SEQ ID NO:1.
27. (New) The method of claim 2, wherein the L1 element comprises SEQ ID NO:1.
28. (New) The method of claim 2, wherein the region of the genome is within 5 million bases on either side of the SLE-associated marker.
29. (New) The method of claim 2, wherein the region of the genome is within 1.7 cM on either side of the SLE-associated marker.

30. (New) The method of claim 3, wherein the L1 element has at least about 98% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
31. (New) The method of claim 3, wherein the L1 element has at least about 99% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
32. (New) The method of claim 3, wherein the L1 element comprises residues 1-884 of SEQ ID NO:1.
33. (New) The method of claim 3, wherein the L1 element comprises SEQ ID NO:1.
34. (New) The method of claim 3, wherein the region of the genome is within 5 million bases on either side of the SLE-associated marker.
35. (New) The method of claim 3, wherein the region of the genome is within 1.7 cM on either side of the SLE-associated marker.
36. (New) A method of identifying candidate genes involved in systemic lupus erythematosus ( SLE ), comprising identifying a gene containing an L1 element in an intronic region or in a 5' or 3' regulatory region, and selecting any gene within 1.7 cM of an SLE-associated marker as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
37. (New) The method of claim 36, wherein the L1 element comprises SEQ ID NO:1.